

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/582,316
Source: IFWP
Date Processed by STIC: 6/19/06

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IFWP

RAW SEQUENCE LISTING

DATE: 06/19/2006

PATENT APPLICATION: US/10/582,316

TIME: 12:21:17

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Output Set: N:\CRF4\06192006\J582316.raw

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3 <110> APPLICANT: Lu and Slee
5 <120> TITLE OF INVENTION: Tumour Suppressor Protein
7 <130> FILE REFERENCE: 68213-02
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/582,316
C--> 9 <141> CURRENT FILING DATE: 2006-06-08
9 <150> PRIOR APPLICATION NUMBER: PCT/GB04/003492
10 <151> PRIOR FILING DATE: 2004-08-13
12 <150> PRIOR APPLICATION NUMBER: 0328690.3
13 <151> PRIOR FILING DATE: 2003-12-10
15 <150> PRIOR APPLICATION NUMBER: 60/554,990
16 <151> PRIOR FILING DATE: 2004-03-19
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 828
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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34 20 25 30
37 Asp Thr Ala Ala Ala Lys Val Asp Glu Leu Thr Lys Gln Leu Glu Ser
38 35 40 45
41 Leu Trp Ser Asp Ser Pro Ala Pro Pro Gly Pro Gln Ala Gly Pro Pro
42 50 55 60
45 Ser Arg Pro Pro Arg Tyr Ser Ser Ser Ser Ile Pro Glu Pro Phe Gly
46 65 70 75 80
49 Ser Arg Gly Ser Pro Arg Lys Ala Ala Thr Asp Gly Ala Asp Thr Pro
50 85 90 95
53 Phe Gly Arg Ser Glu Ser Ala Pro Thr Leu His Pro Tyr Ser Pro Leu
54 100 105 110
57 Ser Pro Lys Gly Arg Pro Ser Ser Pro Arg Thr Pro Leu Tyr Leu Gln
58 115 120 125
61 Pro Asp Ala Tyr Gly Ser Leu Asp Arg Ala Thr Ser Pro Arg Pro Arg
62 130 135 140
65 Ala Phe Asp Gly Ala Gly Ser Ser Leu Gly Arg Ala Pro Ser Pro Arg
66 145 150 155 160
69 Pro Gly Pro Gly Pro Leu Arg Gln Gln Gly Pro Pro Thr Pro Phe Asp
70 165 170 175
73 Phe Leu Gly Arg Ala Gly Ser Pro Arg Gly Ser Pro Leu Ala Glu Gly
74 180 185 190
77 Pro Gln Ala Phe Phe Pro Glu Arg Gly Pro Ser Pro Arg Pro Pro Ala

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81 Thr Ala Tyr Asp Ala Pro Ala Ser Ala Phe Gly Ser Ser Leu Leu Gly
82      210          215          220
85 Ser Gly Gly Ser Ala Phe Ala Pro Pro Leu Arg Ala Gln Asp Asp Leu
86 225          230          235          240
89 Thr Leu Arg Arg Arg Pro Pro Lys Ala Trp Asn Glu Ser Asp Leu Asp
90      245          250          255
93 Val Ala Tyr Glu Lys Lys Pro Ser Gln Thr Ala Ser Tyr Glu Arg Leu
94      260          265          270
97 Asp Val Phe Ala Arg Pro Ala Ser Pro Ser Leu Gln Leu Leu Pro Trp
98      275          280          285
101 Arg Glu Ser Ser Leu Asp Gly Leu Gly Gly Thr Gly Lys Asp Asn Leu
102      290          295          300
105 Thr Ser Ala Thr Leu Pro Arg Asn Tyr Lys Val Ser Pro Leu Ala Ser
106 305          310          315          320
109 Asp Arg Arg Ser Asp Ala Gly Ser Tyr Arg Arg Ser Leu Gly Ser Ala
110      325          330          335
113 Gly Pro Ser Gly Thr Leu Pro Arg Ser Trp Gln Pro Val Ser Arg Ile
114      340          345          350
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118      355          360          365
121 Pro Ile Pro Leu Ser Met Ile Phe Lys Leu Gln Asn Ala Phe Trp Glu
122      370          375          380
125 His Gly Ala Ser Arg Ala Met Leu Pro Gly Ser Pro Leu Phe Thr Arg
126 385          390          395          400
129 Ala Pro Pro Pro Lys Leu Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
130      405          410          415
133 Gln Ser Gln Pro Gln Pro Gln Leu Pro Pro Gln Pro Gln Thr Gln Pro
134      420          425          430
137 Gln Thr Pro Thr Pro Ala Pro Gln His Pro Gln Gln Thr Trp Pro Pro
138      435          440          445
141 Val Asn Glu Gly Pro Pro Lys Pro Pro Thr Glu Leu Glu Pro Glu Pro
142      450          455          460
145 Glu Ile Glu Gly Leu Leu Thr Pro Val Leu Glu Ala Gly Asp Val Asp
146 465          470          475          480
149 Glu Gly Pro Val Ala Arg Pro Leu Ser Pro Thr Arg Leu Gln Pro Ala
150      485          490          495
153 Leu Pro Pro Glu Ala Gln Ser Val Pro Glu Leu Glu Glu Val Ala Arg
154      500          505          510
157 Val Leu Ala Glu Ile Pro Arg Pro Leu Lys Arg Arg Gly Ser Met Glu
158      515          520          525
161 Gln Ala Pro Ala Val Ala Leu Pro Pro Thr His Lys Lys Gln Tyr Gln
162      530          535          540
165 Gln Ile Ile Ser Arg Leu Phe His Arg His Gly Gly Pro Gly Pro Gly
166 545          550          555          560
169 Gly Pro Glu Pro Glu Leu Ser Pro Ile Thr Glu Gly Ser Glu Ala Arg
170      565          570          575
173 Ala Gly Pro Pro Ala Pro Ala Pro Pro Ala Pro Ile Pro Pro Pro Ala
174      580          585          590

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181 Ser Val Leu Arg Lys Ala Gly Ser Pro Arg Lys Ala Arg Arg Ala Arg
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185 Leu Asn Pro Leu Val Leu Leu Leu Asp Ala Ala Leu Thr Gly Glu Leu
186 625      630      635      640
189 Glu Val Val Gln Gln Ala Val Lys Glu Met Asn Asp Pro Ser Gln Pro
190      645      650      655
193 Asn Glu Glu Gly Ile Thr Ala Leu His Asn Ala Ile Cys Gly Ala Asn
194      660      665      670
197 Tyr Ser Ile Val Asp Phe Leu Ile Thr Ala Gly Ala Asn Val Asn Ser
198      675      680      685
201 Pro Asp Ser His Gly Trp Thr Pro Leu His Cys Ala Ala Ser Cys Asn
202      690      695      700
205 Asp Thr Val Ile Cys Met Ala Leu Val Gln His Gly Ala Ala Ile Phe
206 705      710      715      720
209 Ala Thr Thr Leu Ser Asp Gly Ala Thr Ala Phe Glu Lys Cys Asp Pro
210      725      730      735
213 Tyr Arg Glu Gly Tyr Ala Asp Cys Ala Thr Tyr Leu Ala Asp Val Glu
214      740      745      750
217 Gln Ser Met Gly Leu Met Asn Ser Gly Ala Val Tyr Ala Leu Trp Asp
218      755      760      765
221 Tyr Ser Ala Glu Phe Gly Asp Glu Leu Ser Phe Arg Glu Gly Glu Ser
222      770      775      780
225 Val Thr Val Leu Arg Arg Asp Gly Pro Glu Glu Thr Asp Trp Trp Trp
226 785      790      795      800
229 Ala Ala Leu His Gly Gln Glu Gly Tyr Val Pro Arg Asn Tyr Phe Gly
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233 Leu Phe Pro Arg Val Lys Pro Gln Arg Ser Lys Val
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237 <210> SEQ ID NO: 2

238 <211> LENGTH: 3117

239 <212> TYPE: DNA

240 <213> ORGANISM: Homo sapiens

242 <400> SEQUENCE: 2

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247 tcgctggcca tgaaacacat ggatctgaag cagatggagc tggacacggc ggcggccaag      180
249 gtggatgaac tgaccaagca gctggagtcg ctgtgggtcag actctcccgc gcctcctggc      240
251 ccgcaggccg gaccccttc taggcgcgcc cggtagagct ccagctcgat ccctgagccc      300
253 ttccgcagcc gagggtcgcc ccggaaggcg gccaccgacg gcgcagacac cccgttcgga      360
255 cgatcagaga gtgcccacac cctacacccc tacagcccgc tgtcccccaa gggacggccg      420
257 tcgtcgccgc gcaccccgct ctacctgcag ccggacgcct acggcagcct ggaccgcgcg      480
259 acctcgcccc ggccccgcgc cttcgatggc gcaggcagct ccctcgcccg tgcgccttc      540
261 ccgcggcccg ggccaggccc gctccgccag cagggtcccc ccacgccttt cgacttctcg      600
263 ggcgcgcccg gctcccccg cggcagcccc ctggcggagg ggccccaggc cttcttcccc      660
265 gaggctgggc cgtcaccgcg cccccctgcc acagcctacg acgcgccagc gtccgccttc      720
267 gggagctccc tgctaggctc cggcggcagc gcattcgccc cgctctgcg cgcgcaagac      780
269 gacctgacgc tgcgcggcg gcctccgaaa gcctggaacg agtctgacct ggacgtggcg      840

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271 tacgagaaga agccttcgca gacagcgagc tatgaacgcc tggacgtctt cgcaaggcct      900
273 gcctcgccga gcctgcagct gttgccttgg agggagagca gcctggatgg actggggggc      960
275 accggcaagg acaacctcac tagcgccacc ctgccgcgca attacaaggt ctctcctctg     1020
277 gccagcgacc ggcgttcaga cgcggggcagc taccggcgct cgctgggctc cgcggggccg     1080
279 tcgggcactt tgcttcgcag ctggcagccc gtcagccgca tccccatgcc cccctccagc     1140
281 ccccgagcccc gcgggggcccc gcgccagcgt cccatcccccc tcagcatgat cttcaagctg     1200
283 cagaacgcct tctgggagca cggggccagc cgcgccatgc tccctgggtc cccctcttc     1260
285 acccgagcac ccccgcccaa gctgcagccc caaccacaa cacagcccca gccacaatca     1320
287 caaccacagc cccagctgcc cccacagccc cagacccaa cccaaacccc taccagcgc     1380
289 cccagcatc cccaacagac atggccccct gtgaacgaag gaccccccaa acccccacc     1440
291 gagctggagc ctgagccgga gatagagggg ctgctgacac cagtgtgga ggctggcgat     1500
293 gtgatgaag gccctgtagc aaggcctctc agccccacga ggctgcagcc agcactgcca     1560
295 ccggaggcac agtcggtgcc cgagctggag gagggtggac ggggtgttggc ggaaattccc     1620
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313 ctcatcaccg cgggtgccaa tgtcaactcc cccgacagcc acggctggac acccttgca     2160
315 tgcgcggcgt cgtgcaacga cacagtcac tgcattggcg tgggtgcagca cggcgctgca     2220
317 atcttcgcca ccacgctcag cgacggcgcc accgccttcg agaagtgcga cccttaccgc     2280
319 gagggttatg ctgactgcgc cacctacctg gcagacgtcg agcagagtat ggggctgatg     2340
321 aacagcgggg cagtgtacgc tctctgggac tacagcgccg agttcgggga cgagctgtcc     2400
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335 ctgggaaggg ctggaaatca ctggggacag gaaaccactt ccttttgcca aatcagatcc     2820
337 cgtccaaagt gcctcccatg cctaccacca tcatcacatc cccagcaag ccagccacct     2880
339 gccagccggg gcctgggatg ggccaccaca ccactggata ttcttgggag tctactgtga     2940
341 caccatctct cccagcagtc ttggggtctg ggtgggaaac attggtctct accaggatcc     3000
343 ctgccccacc tctccccaat taagtgcctt cacacagctc tggtttaatg tttataaaca     3060
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350 <212> TYPE: PRT
351 <213> ORGANISM: Homo sapiens
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360 20 25 30
363 Val Ala Arg Val Leu Ala Glu Ile Pro Arg Pro Leu Lys Arg Arg Gly
364 35 40 45

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367 Ser Met Glu Gln Ala Pro Ala Val Ala Leu Pro Pro Thr His Lys Lys
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371 Gln Tyr Gln Gln Ile Ile Ser Arg Leu Phe His Arg His Gly Gly Pro
372 65                      70                      75                      80
375 Gly Pro Gly Gly Arg Ser Gln Ser Cys Pro Pro Ser Leu Arg Asp Leu
376                      85                      90                      95
379 Arg Pro Gly Gln Gly Pro Leu Leu Leu Pro His Gln Leu Pro Phe His
380                      100                     105                     110
383 Arg Pro Ala Pro Ser Gln Ser Ser Pro Pro Glu Gln Pro Gln Ser Met
384                      115                     120                     125
387 Glu Met Arg Ser Val Leu Arg Lys Ala Gly Ser Pro Arg Lys Ala Arg
388                      130                     135                     140
391 Arg Ala Arg Leu Asn Pro Leu Val Leu Leu Leu Asp Ala Ala Leu Thr
392 145                      150                      155                      160
395 Gly Glu Leu Glu Val Val Gln Gln Ala Val Lys Glu Met Asn Asp Pro
396                      165                      170                      175
399 Ser Gln Pro Asn Glu Glu Gly Ile Thr Ala Leu His Asn Ala Ile Cys
400                      180                     185                     190
403 Gly Ala Asn Tyr Ser Ile Val Asp Phe Leu Ile Thr Ala Gly Ala Asn
404                      195                     200                     205
407 Val Asn Ser Pro Asp Ser His Gly Trp Thr Pro Leu His Cys Ala Ala
408                      210                     215                     220
411 Ser Cys Asn Asp Thr Val Ile Cys Met Ala Leu Val Gln His Gly Ala
412 225                      230                      235                      240
415 Ala Ile Phe Ala Thr Thr Leu Ser Asp Gly Ala Thr Ala Phe Glu Lys
416                      245                     250                     255
419 Cys Asp Pro Tyr Arg Glu Gly Tyr Ala Asp Cys Ala Thr Tyr Leu Ala
420                      260                     265                     270
423 Asp Val Glu Gln Ser Met Gly Leu Met Asn Ser Gly Ala Val Tyr Ala
424                      275                     280                     285
427 Leu Trp Asp Tyr Ser Ala Glu Phe Gly Asp Glu Leu Ser Phe Arg Glu
428                      290                     295                     300
431 Gly Glu Ser Val Thr Val Leu Arg Arg Asp Gly Pro Glu Glu Thr Asp
432 305                      310                      315                      320
435 Trp Trp Trp Ala Ala Leu His Gly Gln Glu Gly Tyr Val Pro Arg Asn
436                      325                     330                     335
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440                      340                     345                     350
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453 cagccccag ccccgcgggg ccccgcgcca cgcgccatc cccctcagca tgatcttcaa      180
455 gctgcagaac gccttctggg agcacggggc cagccgcgcc atgctccctg ggtccccct      240
457 cttcacccga gcacccccgc ctaagctgca gccccaacca caaccacagc cccagccaca      300
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/582,316

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date